In the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Cancelled)

2. (Currently amended) A ~~The~~ method ~~of claim 1 wherein the amplification comprises performing~~ of determining an angiotensin converting enzyme (ACE) genotype in a sample, comprising:

amplifying DNA in a single ~~polymerase chain reaction~~ amplification reaction from the sample with a first pair of flanking primers that hybridize to nucleic acid sequences flanking an ACE gene sequence, and a third primer that specifically binds to said ACE gene sequence and together with one of the flanking primers forms a second pair of primers; and

detecting a homozygous ACE genotype by the production of one or two amplification products and a heterozygous ACE genotype by the production of three amplification products.

3-39. (Cancelled)

40. (New) The method of claim 2 wherein said amplification reaction is by polymerase chain reaction.

41. (New) The method of claim 2 wherein the sample is a human sample.

42. (New) The method of claim 41 wherein the method distinguishes between genotypes selected from the group consisting of: insertion/insertion, insertion/deletion, deletion/deletion.

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43. (New) The method of claim 41 wherein the DNA is un-degraded DNA.

44. (New) The method of claim 43 wherein the sample is a tissue sample.

45. (New) The method of claim 44 wherein the sample is selected from the group consisting of: blood, cultured cells, cells derived from amniotic fluid, and cells derived from chorionic villi.

46. (New) The method of claim 2 wherein the sample is blood.

47. (New) The method of claim 41 wherein the ACE sequence resides on Intron 16 of chromosome 17q23.

48. (New) The method of claim 41 wherein the ACE sequence is a 287 base pair nonsense DNA domain.

49. (New) The method of claim 41 wherein the first pair of flanking primers have the nucleic acid sequences 5'-CCA TCC TTT CTC CCA TTT CTC T-3' (SEQ ID NO: 1) and 5'-GGA TGG TCT CGA TCT CCT GA-3' (SEQ ID NO: 2); and

the third primer has the nucleic acid sequence 5'-CCT TAG CTC ACC TCT GCT TGT AA-3'(SEQ ID NO: 3).

50. (New) The method of claim 41 wherein the DNA sample is from a source selected from the group consisting of: the endothelium of blood vessels, epithelial cells, blood mononuclear cells, macrophages, male germinal cells, and a biological fluid.

51. (New) The method of claim 41 wherein the nucleic acid products consist of a first nucleic acid fragment of approximately 123 base pairs, a second nucleic acid fragment

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of approximately 157 base pairs, and a third nucleic acid fragment of approximately 410 base pairs.

52. (New) The method of claim 49 wherein the nucleic acid products consist of a first nucleic acid fragment of 123 base pairs, a second nucleic acid fragment of 157 base pairs, and a third nucleic acid fragment of 410 base pairs.

53. (New) The method of claim 52 wherein:

when the first nucleic acid fragment is not present and the second and third nucleic acid fragments are present, the genotype is I/I;

when the first, second, and third nucleic acid fragments are present, the genotype is I/D; and

when the first nucleic acid fragment is present and the second and third nucleic acid fragments are not present, the genotype is D/D.

54. (New) The method of claim 2 wherein the first pair of flanking primers have the nucleic acid sequences 5'-CCA TCC TTT CTC CCA TTT CTC T-3' (SEQ ID NO: 1) and 5'-GGA TGG TCT CGA TCT CCT GA-3' (SEQ ID NO: 2); and

the third primer has the nucleic acid sequence 5'-CCT TAG CTC ACC TCT GCT TGT AA-3' (SEQ ID NO: 3).

55. (New) The method of claim 54 wherein the amplification is by polymerase chain reaction.

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56. (New) The method of claim 55 wherein the method distinguishes between genotypes selected from the group consisting of: insertion/insertion, insertion/deletion, deletion/deletion.

57. (New) The method of claim 55 wherein the ACE sequence resides on Intron 16 of chromosome 17q23.

58. (New) The method of claim 55 wherein the ACE sequence is a 287 base pair nonsense DNA domain.

59. (New) The method of claim 55 wherein the DNA sample is from a source selected from the group consisting of: the endothelium of blood vessels, epithelial cells, blood mononuclear cells, macrophages, male germinal cells, and a biological fluid.

60. (New) The method of claim 55 wherein the nucleic acid products consist of a first nucleic acid fragment of 123 base pairs, a second nucleic acid fragment of 157 base pairs, and a third nucleic acid fragment of 410 base pairs.

61. (New) The method of claim 60 wherein:

when the first nucleic acid fragment is not present and the second and third nucleic acid fragments are present, the genotype is I/I;

when the first, second, and third nucleic acid fragments are present, the genotype is I/D; and

when the first nucleic acid fragment is present and the second and third nucleic acid fragments are not present, the genotype is D/D.

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62. (New) A method for identifying a patient with a heightened risk of suffering from a disease comprising:

determining the angiotensin converting enzyme (ACE) genotype in a sample from the patient by amplifying DNA in a single amplification reaction from the sample with a first pair of flanking primers that hybridize to nucleic acid sequences flanking an ACE gene sequence, the presence of which indicates the presence of a first ACE gene variant, and the absence of which indicates the presence of a second ACE gene variant, and a third primer that specifically binds to said ACE gene sequence and together with one of the flanking primers forms a second pair of primers;

detecting a homozygous ACE genotype by the production of one or two amplification products and a heterozygous ACE genotype by the production of three amplification products; and

correlating the ACE genotype of the patient with a treatment regimen designed to treat or prevent one or more diseases selected from the group consisting of: myocardial infarction, ischemic and idiopathic dilated cardiomyopathy, sudden death in hypertrophic cardiomyopathy, coronary atherosclerosis, and restenosis after percutaneous transluminal coronary angioplasty.

63. (New) The method of claim 62 wherein the treatment regimen is designed to treat myocardial infarction or coronary atherosclerosis.

64. (New) The method of claim 62 wherein the method distinguishes between genotypes selected from the group consisting of: insertion/insertion, insertion/deletion, deletion/deletion.

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65. (New) The method of claim 62 wherein the genotype is determined by detecting the presence or absence of each of three nucleic acid products of the amplification reaction.

66. (New) The method of claim 63 wherein the pair of flanking primers have the nucleic acid sequences 5'-CCA TCC TTT CTC CCA TTT CTC T-3' (SEQ ID NO: 1) and 5'-GGA TGG TCT CGA TCT CCT GA-3' (SEQ. ID NO: 2); and

the third primer has the nucleic acid sequence 5'-CCT TAG CTC ACC TCT GCT TGT AA-3' (SEQ ID NO: 3).

67. (New) A method of determining a genotype for a gene of interest in a sample, comprising:

amplifying DNA in a single amplification reaction from the sample with a first pair of flanking primers that hybridize to nucleic acid sequences flanking a sequence in said gene of interest, the presence of which indicates the presence of a first gene variant, and the absence of which indicates the presence of a second gene variant, and a third primer that specifically binds to said gene sequence and together with one of the flanking primers forms a second pair of primers; and

detecting a homozygous genotype by the production of one or two amplification products and a heterozygous genotype by the production of three amplification products.

68. (New) The method of claim 67 wherein said amplification is by polymerase chain reaction.

69. (New) The method of claim 67 wherein the sample is a human sample.

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70. (New) The method of claim 67 wherein the DNA sample is from a source selected from the group consisting of: the endothelium of blood vessels, epithelial cells, blood mononuclear cells, macrophages, male germinal cells, and a biological fluid.

71. (New) The method of claim 67 wherein the nucleic acid products consist of a first nucleic acid fragment of approximately 123 base pairs, a second nucleic acid fragment of approximately 157 base pairs, and a third nucleic acid fragment of approximately 410 base pairs.

72. (New) The method of claim 67 wherein the nucleic acid products consist of a first nucleic acid fragment of 123 base pairs, a second nucleic acid fragment of 157 base pairs, and a third nucleic acid fragment of 410 base pairs.

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